19. The method of claim 18, wherein the first and second collections of nucleic acids are differentially labeled.

20. The method of claim 18, wherein the first and second collection of nucleic acids comprise the same detectable label.

21. The method of claim 18, wherein the step of removing said hybridized nucleic acids further comprises incubation of the array with nuclease.

22. The method of claim 20, wherein each of the different modified polynucleotide probes is attached to the surface of the substrate in a different predefined region.

23. The method of claim 18, wherein each of the modified polynucleotide probes in a predefined region has a different determinable sequence, and further wherein each probe is at least 4 nucleotides in length.

24. The method of claim 18 further comprising as a last step, incubating the array with an acid solution of pH 1-2 whereby the array is regenerated for reuse.

25. A method of identifying nucleotide differences between the sequence of a target nucleic acid and the sequence of a reference nucleic acid comprising:

(a) providing a substrate comprising different modified polynucleotide probes of known sequence at known locations;

(b) contacting the target nucleic acid with the modified polynucleotide probes attached to the substrate under conditions for high specificity complementary hybridization;

(c) determining which modified polynucleotide probes have hybridized with the target nucleic acid;

(d) removing hybridized target nucleic acid from the polynucleotide probes by incubation of the array with an acid solution of pH 1-2;

(e) contacting the reference nucleic acid with the modified polynucleotide probes attached to the substrate under conditions for high specificity complementary hybridization; and

(f) comparing the sequence of the reference nucleic acid with the sequences of the modified polynucleotide probes that have hybridized with the target nucleic acid and to identify the nucleotide differences between the sequence of the target nucleic acid and the sequence of the reference nucleic acid.

26. The method of claim 25, wherein each of the different modified polynucleotide probes is attached to the surface of the substrate in a different predefined region.

27. The method of claim 26, wherein each of the modified polynucleotide probes in a predefined region has a different determinable sequence, and further wherein each probe is at least 4 nucleotides in length; further wherein the modified oligonucleotides are characterized by a characteristic selected from the group consisting of (a) a binding affinity of at least about 1.25 times that of a corresponding, non-modified oligonucleotide, (b) a pH stability of at least one hour at 37°C at a pH in a range of about 0.5 to 10; and (c) a nuclease resistance of at least twice that of a naturally occurring oligonucleotide having the same sequence and number of bases.

28. The method of claim 25 further comprising as a last step, incubating the array with an acid solution of pH 1-2 whereby the array is regenerated for reuse.

**In the specification:**

**Please replace the paragraph on page 25, lines 11-25, with the following paragraph:**

Oligonucleotides having a sequence unique to that gene are preferably used in the present invention. Different methods may be employed to choose the specific region of the gene to be targeted. A rational design approach may also be employed to choose the optimal oligonucleotide sequence for the hybridization array. Preferably, the region of the gene that is selected is chosen based on the following criteria. First, the sequence that is chosen should yield a oligonucleotide composition that preferably does not cross-hybridize with any other oligonucleotide composition present on the array. Second, the sequence should be chosen such that the oligonucleotide composition has a low probability of cross-hybridizing with an oligonucleotide having a nucleotide sequence found in any other gene, whether or not the gene is to be represented on the array from the same species of origin, e.g., for a human array, the sequence will not be present in any other human genes. As such, sequences that are avoided include those found in: highly expressed gene products, structural RNAs, repeated sequences found in the sample to be tested with the array and sequences found in vectors. A further consideration is to select sequences